

S4 Table. Mutations within the six (low, med, high) samples sequenced to characterize the VPg and eIF4 mutant libraries.

Library sample	eIF4E LOW									
total mutations	60		4	32	26	37	14	5		0
mutant ref.	Mutations	nt Position	INDEL	Transition	Transversion	NS	S	STOP	aa Substitution	aaPosition
430	1		0	0	1	0	1	0	1	0
	AT	162		0	1		1		PP	54
431	5		0	2	3	4	0	1	5	0
	GT	60		0	1	1			LF	20
	GA	230		1	0	1			SN	77
	AT	341		0	1	1			KM	114
	GT	575		0	1	1			SI	192
	GA	590		1	0			1	STOP	197
432	4		0	1	3	2	1	1	4	0
	CA	113		0	1	1			TN	38
	TA	329		0	1			1	STOP	110
	AG	440		1	0	1			YC	147
	AC	555		0	1		1		AA	185
433	1		1	0	0	0	0	0	1	0
	INSERTION	536	1	0	0					179
434	2		0	0	2	1	1	0	2	0
	TA	180		0	1		1		TT	60
	GC	379		0	1	1			AP	127,0
435	1		0	1	0	0	1	0	1	0,0
	GA	129		1	0		1		SS	43
436	4		0	2	2	3	0	1	4	0,0
	TA	120		0	1	1			DE	40
	TA	134		0	1			1	STOP	45

	TC	175		1	0	1			WR	59,0
	GA	553		1	0	1			AT	185,0
437	7		0	5	2	5	2	0	7	0,0
	AG	47		1	0	1			EG	16
	AT	366		0	1	1			ED	122
	AT	398		0	1	1			KI	133
	CT	429		1	0		1		TT	143
	AG	487		1	0	1			IV	163,0
	GA	496		1	0	1			AT	166,0
	TC	600		1	0		1		FF	200
439	2		1	1	0	1	0	0	2	0,0
	INSERTION	100	1	0	0					33
	CT	428		1	0	1			TI	143
406	1		0	1	0	1	0	0	1	0,0
	TC	536		1	0	1			LS	179
407	4		1	2	1	3	0	0	4	0,0
	GA	95		1	0	1			GD	32
	GA	217		1	0	1			AT	73,0
	INSERTION	461	1	0	0					154
	GT	591		0	1	1			WC	197
408	0		0	0	1	0	0	0	0	0
				0	1					0
409	0		0	0	1	0	0	0	0	0
				0	1					0
410	1		0	1	0	0	1	0	1	0
	GA	585		1	0		1		KK	195
15	0		0	0	0	0	0	0	0	0
										0
16	1		0	1	0	0	1	0	1	0
	TC	270		1	0		1		DD	90

17	2		0	2	0	1	1	0	2	0
	AG	215		1	0	1			QR	72
	TC	282		1	0		1		AA	94
18	3		1	0	2	2	0	0	3	0
	INSERTION	278	1	0	0					93
	GC	335		0	1	1			CS	112
	GC	424		0	1	1			DH	142,0
19	1		0	0	1	0	0	1	1	0
	AT	526		0	1			1	STOP	176,0
19BIS	0		0	0	0	0	0	0	0	0
										0
20	2		0	2	0	1	0	1	2	0
	GA	185		1	0			1	STOP	62
	CT	343		1	0	1			HY	115,0
21	0		0	0	0	0	0	0	0	0
										0
22	0		0	0	0	0	0	0	0	0
										0
23	1		0	1	0	0	1	0	1	0
	TC	408		1	0		1		FF	136
24	1		0	1	0	1	0	0	1	0
	GA	52		1	0	1			VM	18,0
25	1		0	1	0	1	0	0	1	0
	GA	508		1	0	1			VI	170,0
26	2		0	2	0	2	0	0	2	0
	GA	64		1	0	1			AT	21,3
	GA	262		1	0	1			VI	88,0
27	1		0	1	0	0	1	0	1	0
	TC	78		1	0		1		DD	26
28	2		0	2	0	1	1	0	2	0

	AG	215		1	0	1			QR	72
	TC	282		1	0		1		AA	94
29	0		0	0	0	0	0	0	0	0
										0
30	5		0	2	3	4	1	0	5	0
	AT	141		0	1	1			KN	47
	GA	156		1	0		1		KK	52
	AT	213		0	1	1			KN	71
	CT	281		1	0	1			AV	94
	CA	343		0	1	1			HN	115,0
31	2		0	0	2	1	1	0	2	0
	AT	174		0	1		1		SS	58
	TA	602		0	1	1			LQ	201
32	3		0	1	2	3	0	0	3	0
	AC	528		0	1	1			KN	176
	GC	565		0	1	1			AP	189,0
	AG	641		1	0	1			DG	214

TA	5
AT	8
CG	0
GC	4
TG	0
GT	3
GA	14
AG	6
CA	2
AC	2
TC	8
CT	4

INSERTION 4
 DELETION 0

Library sample	VPg LOW									
total mutations	25	0	1	15	10	16	8	0		0
Mutant ref	Mutations	nt Position	INDEL	Transition	Transversion	NS	S	STOP	aa substitution	aa Position
1	0		0	0	0	0	0	0	0	0
2	1		0	1	0	0	1	0	1	0
	GA	354		1	0		1		LL	118
3	0		0	0	0	0	0	0	0	0
4	2		0	2	0	1	1	0	2	0
	GA	50		1	0	1			RH	17
	CT	78		1	0		1		DD	26
5	0		0	0	0	0	0	0	0	0
6	1		0	1	0	1	0	0	1	0
	GA	406		1	0	1			AT	136,0
7	5		0	1	4	3	2	0	5	0
	AG	163		1	0	1			KE	55,0
	AT	249		0	1		1		AA	83
	TA	273		0	1		1		AA	91
	TA	375		0	1	1			HQ	125
	GC	406		0	1	1			AP	136,0
8	2		1	1	1	0	1	0	2	0
	AG	291		1	0		1		QQ	97
	INSERTION	462	1	0	1					154

9	0		0	0	0	0	0	0	0	0	0
											0
10	0		0	0	0	0	0	0	0	0	0
											0
11	2		0	0	2	2	0	0	2	0	0
	CA	223		0	1	1			QK		75,0
	CA	242		0	1	1			TN		81
12	0		0	0	0	0	0	0	0	0	0
											0
13	1		0	1	0	1	0	0	1	0	0
	GA	334		1	0	1			EK		112,0
14	0		0	0	0	0	0	0	0	0	0
											0
15	0		0	0	0	0	0	0	0	0	0
											0
16	1		0	1	0	1	0	0	1	0	0
	GA	445		1	0	1			VI		149,0
17	1		0	1	0	1	0	0	1	0	0
	CT	373		1	0	1			HY		125,0
18	1		0	1	0	1	0	0	1	0	0
	GA	50		1	0	1			RH		17
19	0		0	0	0	0	0	0	0	0	0
											0
20	0		0	0	0	0	0	0	0	0	0
											0
21	1		0	1	0	0	1	0	0	0	0
	GA	354		1	0		1		LL		118
22	1		0	0	1	1	0	0	1	0	0
	CA	515		0	1	1			AD		172
23	1		0	1	0	1	0	0	1	0	0

	CT	559		1	0	1				HY	187,0
24	1		0	1	0	1	0	0	0	1	0
	GA	232		1	0	1				DN	78,0
25	0		0	0	0	0	0	0	0	0	0
											0
26	0		0	0	0	0	0	0	0	0	0
											0
27	0		0	0	0	0	0	0	0	0	0
											0
29	0		0	0	0	0	0	0	0	0	0
											0
30	3		0	1	2	1	2	0	0	3	0
	TA	67		0	1	1				FI	23,0
	AT	456		0	1		1			KN	152
	AG	552		1	0		1			EE	184
31	0		0	0	0	0	0	0	0	0	0
											0
32	1		0	1	0	1	0	0	0	1	0
	CT	206		1	0	1				TI	69

TA 3
 AT 2
 CG 0
 GC 1
 TG 0
 GT 0
 GA 8
 AG 3
 CA 3
 AC 0

TC 0
 CT 4
 INSERTION 1
 DELETION 0

Library sample eIF4E med

total mutations		78	0	60	18	62	14	2	0	
Mutant ref	Mutations	nt Position	INDEL	Transition	Transversion	NS	S	STOP	aa substitution	aa Position
1	0		0	0	0	0	0	0	0	0
2	1		0	0	1	1	0	0	1	0
	GT	540		0	1	1			WC	180
3	3		0	2	1	3	0	0	3	0
	CT	138		1	0	1			SS	46
	CA	436		0	1	1			LI	146,0
	CT	551		1	0	1			AV	184
4	5		0	4	1	4	1	0	5	0
	GA	46		1	0	1			EK	16,0
	GA	123		1	0		1		TT	41
	AT	216		0	1	1			QH	72
	GA	373		1	0	1			VI	125,0
	AG	560		1	0	1			EG	187
5	1		0	1	0	0	1	0	1	0
	GA	168		1	0		1		EE	56
6	3		0	3	0	2	1	0	3	0
	CT	161		1	0	1			PL	54
	CT	301		1	0	1			PS	101,0
	CT	576		1	0		1		SS	192
7	3		0	3	0	1	2	0	3	0

	GA	431		1	0	1			SN	144
	TC	618		1	0		1		SS	206
	CT	654		1	0		1		LL	218
8	3		0	2	1	2	0	1	3	0
	GA	185		1	0			1	STOP	62
	GT	581		0	1	1			GV	194
	TC	625		1	0	1			FL	209,0
9	1		0	0	1	1	0	0	1	0
	AT	242		0	1	1			NI	81
10	3		0	3	0	3	0	0	3	0
	GA	190		1	0	1			DN	64,0
	GA	496		1	0	1			AT	166,0
	GA	508		1	0	1			VI	170,0
11	0		0	0	0	0	0	0	0	0
										0
12	3		0	2	1	3	0	0	3	0
	CT	260		1	0	1			TI	87
	CT	323		1	0	1			AV	108
	CA	422		0	1	1			SY	141
13	1		0	1	0	0	1	0	1	0
	GA	537		1	0		1		LL	179
14	0		0	0	0	0	0	0	0	0
										0
15	8		0	6	2	6	2	0	8	0
	CT	113		1	0	1			TI	38
	GA	217		1	0	1			AT	73,0
	GC	244		0	1	1			VL	82,0
	TC	293		1	0	1			IT	98
	TC	423		1	0		1		SS	141
	GA	585		1	0		1		KK	195

	GA	613		1	0	1			DN	205,0
	GC	643		0	1	1			AP	215,0
16	3		0	3	0	1	2	0	3	0
	CT	301		1	0	1			PS	101,0
	CT	432		1	0		1		SS	144
	TC	504		1	0		1		VV	168
17	2		0	2	0	2	0	0	2	0
	GA	70		1	0	1			EK	24,0
	CT	122		1	0	1			TM	41
18	0		0	0	0	0	0	0	0	0
										0,0
19	2		0	2	0	2	0	0	2	0
	CT	251		1	0	1			TI	84
	GA	316		1	0	1			VM	106,0
20	1		0	1	0	1	0	0	1	0
	GA	325		1	0	1			DN	109,0
21	4		0	2	2	3	1	0	4	0
	TA	120		0	1	1			DE	40
	AT	321		0	1		1		GG	107
	GA	431		1	0	1			SN	144
	GA	550		1	0	1			AT	184,0
22	2		0	2	0	0	1	1	2	0
	GA	185		1	0			1	STOP	62
	GA	309		1	0		1		KK	103
23	2		0	1	1	2	0	0	2	0
	AG	41		1	0	1			EG	14
	GC	230		0	1	1			ST	77
24	0		0	0	0	0	0	0	0	0
										0
25	3		0	3	0	2	1	0	3	0

	GA	85		1	0	1			VI	29,0
	GA	379		1	0	1			AT	127,0
	TC	423		1	0		1		SS	141
26	5		0	2	3	5	0	0	5	0
	CT	125		1	0	1			TM	42
	CT	251		1	0	1			TI	84
	CA	281		0	1	1			AD	94
	TA	572		0	1	1			VD	191
	AT	647		0	1	1			KM	216
27	1		0	0	1	1	0	0	1	0
	CG	343		0	1	1			HD	115,0
28	3		0	2	1	3	0	0	3	0
	AC	108		0	1	1			ED	36
	CT	169		1	0	1			HY	57,0
	GA	227		1	0	1			GD	76
29	2		0	0	2	1	1	0	2	0
	AC	50		0	1	1			KI	17
	TA	102		0	1		1		II	34
30	5		0	5	0	5	0	0	5	0
	CT	65		1	0	1			AV	22
	TC	253		1	0	1			FL	85,0
	GA	305		1	0	1			SN	102
	CT	497		1	0	1			AV	166
	GA	520		1	0	1			GR	174,0
31	5		0	5	0	5	0	0	5	0
	GA	79		1	0	1			DN	27,0
	CT	161		1	0	1			PL	54
	GA	313		1	0	1			VI	105,0
	CT	428		1	0	1			TI	143
	CT	443		1	0	1			TM	148

32		3		0		3		0		0		3		0	
	CT	169		1	0	1							HY	57,0	
	GA	502		1	0	1							VI	168,0	
	AG	646		1	0	1							KE	216,0	
TA		3													
AT		4													
CG		1													
GC		3													
TG		0													
GT		2													
GA		28													
AG		3													
CA		3													
AC		2													
TC		7													
CT		22													
INSERTION		0													
DELETION		0													

Library sample	VPg MED									
total mutations	66	4	31	36	41	21	0	0	0	0
Mutant ref	Mutations	nt Position	INDEL	Transition	Transversion	NS	S	STOP	aa substitution	aa Position
312	2		0	2	0	1	1	0	2	0
	GA	159		1	0	1			MI	53,0
	TC	198		1	0		1		FF	66,0

311	2		0	1	1	1	1	0	2	0
	TA	278		0	1	1			IN	93,0
	TC	421		1	0		1		LL	141,0
310	2		1	0	2	1	0	0	2	0
	INSERTION	223	1	0	1					74,3
	TA	300		0	1	1			FL	100,0
308	2		0	1	1	2	0	0	2	0
	GA	88		1	0	1			DN	30,0
	AT	431		0	1	1			HL	144,0
307	4		0	2	2	1	3	0	4	0
	AG	258		1	0		1		EE	86,0
	GT	366		0	1		1		TT	122,0
	GA	414		1	0		1		KK	138,0
	GT	509		0	1	1			GV	170,0
305	3		0	2	1	1	2	0	3	0
	TC	39		1	0		1		FF	13,0
	CA	186		0	1	1			NK	62,0
	GA	309		1	0		1		VV	103,0
304	5		0	1	4	3	2	0	5	0
	GT	154		0	1	1			GC	52,0
	TA	243		0	1		1		TT	81,0
	GT	318		0	1	1			KN	106,0
	TA	425		0	1	1			MK	142,0
	GA	498		1	0		1		LL	166,0
303	4		0	1	3	4	0	0	4	0
	CA	49		0	1	1			RS	17,0
	AG	145		1	0	1			TA	49,0
	GT	170		0	1	1			SI	57,0
	TA	467		0	1	1			IN	156,0
302	3		1	2	1	2	0	0	3	0

	TC	95		1	0	1			IT	32,0
	AG	290		1	0	1			QR	97,0
	INSERTION	546	1	0	1					182,0
301	3		0	0	3	3	0	0	3	0
	TA	254		0	1	1			IK	85,0
	AT	473		0	1	1			KI	158,0
	AT	533		0	1	1			KM	178,0
330	6		0	2	4	5	1	0	6	0
	TA	234		0	1	1			DE	78,0
	AT	367		0	1	1			SC	123,0
	TA	378		0	1		1		AA	126,0
	AG	380		1	0	1			YC	127,0
	AT	431		0	1	1			HL	144,0
	GA	535		1	0	1			DN	179,0
329	5		0	4	1	3	2	0	5	0
	CT	186		1	0		1		NN	62,0
	AG	313		1	0	1			RG	105,0
	AT	326		0	1	1			EV	109,0
	GA	366		1	0		1		TT	122,0
	AG	413		1	0	1			KR	138,0
328	3		0	2	1	2	1	0	3	0
	TA	108		0	1	1			FL	36,0
	GA	354		1	0		1		LL	118,0
	CT	365		1	0	1			TM	122,0
326	4		0	1	3	3	1	0	4	0
	CA	147		0	1		1		TT	49,0
	CG	149		0	1	1			TR	50,0
	TA	268		0	1	1			YN	90,0
	CT	343		1	0	1			PS	115,0
325	0		0	0	1	0	0	0	0	0

				0	1					
324	5		1	3	2	2	2	0	5	0
	INSERTION	199	1	0	1					66,3
	GC	247		0	1	1			AP	83,0
	AG	438		1	0		1		PP	146,0
	CT	496		1	0		1		LL	166,0
	AG	544		1	0	1			KE	182,0
323	3		0	1	2	3	0	0	3	0
	GT	122		0	1	1			RM	41,0
	AT	362		0	1	1			NI	121,0
	CT	511		1	0	1			PS	171,0
322	2		1	0	2	1	0	0	2	0
	TA	211		0	1	1			YN	71,0
	DELETION	411	1	0	1					137,0
321	6		0	5	1	2	4	0	6	0
	AG	93		1	0		1		TT	31,0
	TC	218		1	0	1			FS	73,0
	CT	402		1	0		1		DD	134,0
	AG	405		1	0		1		KK	135,0
	CG	428		0	1	1			PR	143,0
	GA	489		1	0		1		EE	163,0
320	2		0	1	1	1	1	0	2	0
	TA	360		0	1	1			SR	120,0
	AG	405		1	0		1		KK	135,0

TA 12
AT 7
CG 2
GC 1
TG 0

GT	6
GA	9
AG	11
CA	3
AC	0
TC	5
CT	6
INSERTION	3
DELETION	1

Library sample	eIF4E HIGH									
total mutations	223	2	11	93	77	155	44	13	0	
Mutant ref	Mutations	nt Position	INDEL	Transition	Transversion	NS	S	STOP	aa substitution	aa Position
1	5		0	3	2	4	1	0	5	0
	AT	67		0	1	1			NY	23,0
	GA	126		1	0		1		TT	42
	TA	490		0	1	1			CS	164,0
	CT	497		1	0	1			AV	166
	GA	617		1	0	1			SN	206
1'	13		1	3	3	8	4	0	13	0
	AT	107		0	1	1			EV	36
	AT	112		0	1	1			TS	28,0
	AG	139		1	0	1			KE	47,0
	GA	148		1	0	1			AT	50,0
	CT	157		1	0	1			HY	53,0

	CG	221	0	1	1			AG	74
	DELETION	238	1						80,0
	TA	279	0	1			1	GG	93
	GT	379	0	1	1			AS	127,0
	GA	444	1	0			1	TT	148
	TC	450	1	0			1	LL	150
	GA	502	1	0	1			VI	168,0
	GT	603	0	1			1	LL	201
2'	9	0	3	2	8	1	0	9	0
	CA	44	0	1	1			AD	15
	AG	124	1	0	1			TA	42,0
	AT	286	0	1	1			NY	96,0
	GA	404	1	0	1			SN	135
	CT	410	1	0	1			SL	137
	AT	480	0	1	1			ED	160
	GT	499	0	1	1			VL	167,0
	TC	633	1	0			1	FF	211
	AT	677	0	1	1			YF	226
3	4	0	5	4	4	0	0	4	0
	AT	99	0	1	1			ED	33
	AG	154	1	0	1			KE	52,0
	TA	437	0	1	1			LQ	146
	AT	486	0	1	1			ED	162
3'	9	1	4	1	3	4	1	9	0
	CT	231	1	0			1	SS	77
	AG	241	1	0	1			ND	81,0
	AT	267	0	1	1			ED	89
	GA	309	1	0			1	KK	103
	GA	342	1	0			1	KK	114
	AT	358	0	1				1 STOP	120,0

INSERTION		400	1						134,0
	CT	612		1	0		1	SS	204
	AG	628		1	0	1		IV	210,0
4	6		0	2	3	4	1	1	6
	AG	151		1	0	1		TA	51,0
	TG	310		0	1	1		LV	104,0
	TA	509		0	1	1		VD	170
	AG	660		1	0		1	RR	220
	TA	663		0	1	1		NK	221
	CG	678		0	1			1 STOP	226
4'	0								
									0
5	6		0	4	1	5	1	0	6
	CT	125		1	0	1		TM	42
	CG	258		0	1		1	SS	86
	AG	382		1	0	1		ND	128,0
	GA	386		1	0	1		GE	129
	GA	402		1	0	1		MI	134
	TA	426		0	1	1		DE	142
5'	6		0	3	2	5	1	0	6
	GA	106		1	0	1		EK	36,0
	CA	113		0	1	1		TN	38
	GC	190		0	1	1		DH	64,0
	GA	404		1	0	1		SN	135
	GA	444		1	0		1	TT	148
	AT	480		0	1	1		ED	160
6	5		0	1	4	4	1	0	5
	GT	48		0	1	1		ED	16
	AT	61		0	1	1		NY	21,0
	GT	402		0	1	1		MI	134

	AT	485	0	1	1			EV	162	
	TC	672	1	0			1	NN	224	
6'	5		0	0	5	4	1	0	5	0
	AT	178	0	1	1			TS	60,0	
	TA	184	0	1	1			WR	62,0	
	GC	316	0	1	1			VL	106,0	
	AT	348	0	1	1			KN	116	
	AT	357	0	1			1	PP	119	
7	0									
									0	
7'	8		1	3	1	6	0	1	8	0
	GT	106	0	1				1 STOP	36,0	
	CT	128	1	0		1		SL	43	
	DELETION	155	1						52	
	GA	220	1	0	1			AT	74,0	
	GA	278	1	0	1			GD	93	
	AG	365	1	0	1			EG	122	
	AT	560	0	1	1			EV	187	
	CT	566	1	0	1			AV	189	
8	5		0	3	2	4	1	0	5	0
	TA	81	0	1	1			DE	27	
	CA	214	0	1	1			QK	72,0	
	CT	240	1	0			1	RR	80	
	GA	424	1	0	1			DN	142,0	
	TC	572	1	0	1			VA	191	
8'	6		0	2	3	3	3	0	6	0
	TA	189	0	1	1			FL	63	
	CT	300	1	0			1	HH	100	
	GC	316	0	1	1			VL	106,0	
	TC	492	1	0			1	CC	164	

	AT	501	0	1		1		VV	167
	TG	535	0	1		1		LV	179,0
10	5		0	1	4	3	1	1	5
	GA	224	1	0				1 STOP	75
	AT	382	0	1		1		NY	128,0
	TA	465	0	1		1		HQ	155
	AT	505	0	1		1		SC	169,0
	AT	645	0	1			1	AA	215
11	6		0	0	5	6	0	0	6
	AT	143	0	1		1		EV	48
	GT	424	0	1		1		DY	142,0
	CG	445	0	1		1		LV	149,0
	GC	508	0	1		1		VL	170,0
	GC	637	0	1		1		DH	213,0
	GA	650	1	0		1		RK	217
12	6		0	3	2	3	2	1	6
	GT	37	0	1		1		DY	13,0
	TC	270	1	0			1	DD	90
	CA	410	0	1				1 STOP	137
	AG	522	1	0			1	GG	174
	TC	599	1	0		1		FS	200
	AG	671	1	0		1		NS	224
13	5		0	3	2	3	1	1	5
	GA	129	1	0			1	SS	43
	GA	224	1	0				1 STOP	75
	GA	506	1	0		1		SN	169
	CG	563	0	1		1		TR	188
	TA	599	0	1		1		FY	200
14	6		0	2	3	5	1	0	6
	AC	61	0	1		1		NH	21,0

	CT	152	1	0	1			TI	51	
	TC	172	1	0	1			SP	58,0	
	AT	267	0	1	1			ED	89	
	GT	590	0	1	1			WL	197	
	CT	636	1	0			1	HH	212	
15	13		1	1	4	7	3	2	13	0
	AT	150	0	1			1	AA	50	
	TC	237	1	0			1	LL	79	
	AT	332	0	1		1		HL	111	
	TA	441	0	1				1 STOP	147	
	CG	497	0	1		1		AG	166	
	GT	514	0	1		1		GC	172,0	
	DELETION	524	1						175	
	GT	564	0	1			1	TT	188	
	AT	577	0	1		1		IF	193,0	
	AG	593	1	0		1		KR	198	
	AC	641	0	1		1		DA	214	
	AT	646	0	1				1 STOP	216,0	
	GC	682	0	1		1		VL	228,0	
16	11		0	3	2	6	3	2	11	0
	AG	112	1	0		1		TA	37	
	GA	156	1	0			1	KK	52	
	CA	233	0	1				1 STOP	78	
	TC	252	1	0			1	TT	84	
	CA	356	0	1		1		PQ	119	
	GA	389	1	0		1		GE	130	
	AG	430	1	0		1		SG	144,0	
	CA	463	0	1		1		HN	155,0	
	AT	592	0	1				1 STOP	198,0	
	CT	615	1	0			1	DD	205	

	AT	656	0	1	1			DV	219	
19	3		0	6	3	3	0	0	3	0
	GT	313	0	1	1			VF	105,0	
	GT	591	0	1	1			WC	197	
	AG	635	1	0	1			HR	212	
20	8		1	4	1	5	1	1	8	0
	AG	119	1	0	1			DG	40	
	AG	139	1	0	1			KE	47,0	
	TC	329	1	0	1			LS	110	
	TA	350	0	1	1			IN	117	
	GA	354	1	0			1	EE	118	
	GA	395	1	0				1 STOP	132	
	CA	554	0	1	1			AE	185	
	DELETION	647	1						216	
21	5		0	3	2	4	1	0	5	0
	TG	120	0	1	1			DE	40	
	TA	270	0	1	1			DE	90	
	GA	386	1	0	1			GE	129	
	TC	421	1	0	1			SP	141,0	
	CT	657	1	0			1	DD	219	
22	6		0	4	1	6	0	0	6	0
	AT	41	0	1	1			EV	14	
	GA	64	1	0	1			AT	22,0	
	CT	152	1	0	1			TI	51	
	TC	253	1	0	1			FL	85,0	
	TC	274	1	0	1			WR	92,0	
	GT	648	0	1	1			KN	216	
23	5		1	1	3	3	0	1	5	0
	CT	74	1	0	1			AV	25	
	TA	333	0	1	1			HQ	111	

	CA	410		0	1				1 STOP	137
	CA	576		0	1		1		SR	192
	DELETION	633	1							211
24	11		1	5	0	8	1	1	11	0
	AG	154		1	0		1		KE	52,0
	CT	196		1	0		1		PS	66,0
	TC	219		1	0			1	AA	73
	GA	220		1	0		1		AT	74,0
	GA	363		1	0				1 STOP	121
	AT	365		0	1		1		EV	122
	DELETION	413	1							138
	AT	529		0	1		1		IL	177,0
	AT	548		0	1		1		NI	183
	AT	577		0	1		1		IF	193,0
	CT	673		1	0		1		RC	225,0
27	11		1	4	1	8	2	0	11	0
	CA	160		0	1		1		PT	54,0
	TC	163		1	0			1	LL	55,0
	CT	281		1	0		1		AV	94
	CT	463		1	0		1		HY	155,0
	GA	514		1	0		1		GS	172,0
	CT	551		1	0		1		AV	184
	GC	565		0	1		1		AP	189,0
	DELETION	647	1							216
	TA	653		0	1		1		LH	218
	CT	660		1	0			1	DD	220
	AT	657		0	1		1		RS	219
28	6		0	2	3	6	0	0	6	0
	AG	131		1	0		1		YC	44
	TA	270		0	1		1		DE	90

	AT	383		0	1		1		NI	128
	GC	416		0	1		1		GA	139
	TC	470		1	0		1		FS	157
	CT	497		1	0		1		AV	166
29	3		1	5	3	0	2	0	3	0
	GA	234		1	0			1	SS	78
	GA	585		1	0			1	KK	195
	DELETION	647		1						216
30	10	2	2	3	2	4	4	0	10	-2
	GT	51		0	1		1		KN	17
	AG	55		1	0		1		KE	19,0
	GA	72		1	0			1	EE	24
	TA	86		0	1		1		VD	29
	GA	278		1	0		1		GD	93
	AG	324		1	0			1	AA	108
	TA	489		0	1			1	II	163
	DELETION	529		1						177,0
	TC	549		1	0			1	NN	183
	DELETION	647		1						216
31	8		0	3	2	6	2	0	8	0
	AG	119		1	0		1		DG	40
	CT	157		1	0		1		HY	53,0
	CA	295		0	1		1		HN	99,0
	AT	398		0	1		1		KI	133
	TC	489		1	0			1	II	163
	CT	627		1	0			1	FF	209
	AT	647		0	1		1		KM	216
	CA	652		0	1		1		LI	218,0
32	8		0	4	1	7	1	0	8	0
	GA	88		1	0		1		EK	30,0

GA	230	1	0	1		SN	77
GA	244	1	0	1		VI	82,0
CG	443	0	1	1		TR	148
TC	534	1	0		1	SS	178
CG	566	0	1	1		AG	189
GA	622	1	0	1		GS	208,0
TA	642	0	1	1		DE	214

TA	20
AT	38
CG	8
GC	8
TG	3
GT	15
GA	38
AG	22
CA	13
AC	2
TC	20
CT	25
INSERTION	1
DELETION	10

Library sample	VPg HIGH								
total mutations	229	0	12	120	107	156	52	9	0

Mutant ref	Mutations	nt Position	INDEL	Transition	Transversion	NS	S	STOP	aa substitution	aa Position
1	8		0	6	2	5	3	0	8	0
	GA	65		1	0	1			GD	22
	AG	140		1	0	1			KR	47
	TA	152		0	1	1			VD	51
	TC	156		1	0		1		GG	52
	CT	162		1	0		1		GG	54
	GC	414		0	1	1			KN	138
	TC	475		1	0	1			FL	159,0
	GA	489		1	0		1		EE	163
2	7		2	1	6	3	1	1	7	0
	DELETION	155	1	0	1					52
	AT	195		0	1		1		GG	65
	AG	313		1	0	1			RG	105,0
	CA	369		0	1	1			SR	123
	AT	370		0	1	1			IL	124,0
	DELETION	434	1	0	1					145
	TA	450		0	1			1 STOP		150
3	5		2	1	4	3	0	0	5	0
	DELETION	65	1	0	1					22
	AT	258		0	1	1			ED	86
	DELETION	279	1	0	1					93
	AG	372		1	0	1			IM	124
	GT	386		0	1	1			RM	129
4	5		0	3	2	5	0	0	5	0
	GC	265		0	1	1			VL	89,0
	TC	383		1	0	1			FS	128
	AG	473		1	0	1			KR	158
	CA	479		0	1	1			PH	160
	AG	527		1	0	1			NS	176

5	5	0	3	2	4	1	0	5	0
	GA	376	1	0	1			AT	126,0
	TA	378	0	1	1			AT	126
	GC	504	0	1	1			QH	168
	GA	517	1	0	1			VM	173,0
	TC	561	1	0		1		HH	187
6	6	0	4	2	5	1	0	6	0
	GA	65	1	0	1			GD	22
	AC	83	0	1	1			NT	28
	CT	149	1	0	1			TI	50
	TC	234	1	0		1		DD	78
	CT	242	1	0	1			TI	81
	GC	256	0	1	1			EQ	86,0
7	11	0	5	6	6	3	2	11	0
	AT	124	0	1				1 STOP	42,0
	AT	139	0	1				1 STOP	47,0
	CT	180	1	0		1		FF	60
	AT	204	0	1		1		PP	68
	CT	267	1	0		1		VV	89
	GC	315	0	1	1			RS	105
	AT	326	0	1	1			EV	109
	GC	340	0	1	1			ER	114,0
	AG	341	1	0	1			ER	114
	GA	469	1	0	1			AT	157,0
	AG	548	1	0	1			QR	183
8	8	2	5	3	3	3	0	8	0
	GA	57	1	0		1		KK	19
	DELETION	110	1	0	1				37
	TA	118	0	1	1			YN	40,0
	AG	133	1	0	1			KE	45,0

	CT	180		1	0		1		FF	60
	TC	196		1	0		1		FL	66,0
	DELETION	223	1	0	1					75,0
	CT	240		1	0		1		FF	80
9	6		0	4	2	5	1	0	6	0
	CT	42		1	0		1		RR	14
	CT	47		1	0		1		AV	16
	GA	52		1	0		1		DN	18,0
	GT	281		0	1		1		RM	94
	GA	400		1	0		1		DN	134,0
	AC	405		0	1		1		KN	135
10	4		0	3	1	3	1	0	4	0
	GA	154		1	0		1		GS	52,0
	CT	377		1	0		1		AV	126
	AT	494		0	1		1		EV	165
	AG	552		1	0			1	EE	184
14	8		0	2	6	7	1	0	8	0
	GA	99		1	0			1	EE	33
	GC	155		0	1		1		GA	52
	GT	176		0	1		1		RI	59
	GT	368		0	1		1		SI	123
	AT	405		0	1		1		KN	135
	AC	466		0	1		1		IL	156,0
	TC	491		1	0		1		FS	164
	CG	512		0	1		1		PR	171
15	7		0	1	6	6	1	0	7	0
	AT	80		0	1		1		NI	27
	AT	225		0	1		1		QH	75
	CT	248		1	0		1		AV	83
	CA	351		0	1			1	AA	117

	GC	386	0	1	1			RT	129	
	GC	485	0	1	1			RT	162	
	AT	499	0	1	1			RW	167,0	
16	14		0	8	6	8	5	1	14	0
	AT	44	0	1	1			HL	15	
	AT	121	0	1	1			RW	41,0	
	CA	147	0	1			1	TT	49	
	CT	242	1	0	1			TI	81	
	AT	316	0	1				1 STOP	106,0	
	GA	376	1	0	1			AI	126,0	
	CT	377	1	0	1			AI	126	
	TC	399	1	0			1	SS	133	
	TC	425	1	0	1			MT	142	
	AT	431	0	1	1			HL	144	
	CT	453	1	0			1	DD	151	
	AG	486	1	0			1	RR	162	
	TA	491	0	1	1			FY	164	
	AG	552	1	0			1	EE	184	
17	9		1	5	3	7	1	0	9	0
	AT	72	0	1	1			ED	24	
	AG	96	1	0	1			IM	32	
	AG	262	1	0	1			ND	88,0	
	TG	393	0	1	1			DE	131	
	TC	409	1	0			1	LL	137,0	
	AG	461	1	0	1			NS	154	
	GA	469	1	0	1			AT	157,0	
	CG	511	0	1	1			PA	171,0	
	DELETION	535	1	0					179,0	
18	12		1	9	2	9	1	1	12	0
	GA	41	1	0	1			RH	14	

CT	42		1	0		1			RH	14
AT	86		0	1		1			DV	29
AG	157		1	0		1			MV	53,0
GC	170		0	1		1			ST	57
TC	211		1	0		1			YH	71,0
DELETION	222	1	0							74
TC	360		1	0			1		SS	120
GA	400		1	0		1			DN	134,0
CT	402		1	0		1			DN	134
AG	434		1	0		1			NS	145
CT	502		1	0				1	STOP	168,0
19	11	0	8	3	8	3	0	11	0	
TC	107		1	0		1			FS	36
GA	154		1	0		1			GS	52,0
GA	259		1	0		1			EK	87,0
GA	309		1	0			1		VV	103
TA	320		0	1		1			MK	107
AG	342		1	0			1		EE	114
AT	361		0	1		1			NY	121,0
CT	365		1	0		1			TM	122
CT	402		1	0			1		DD	134
AT	455		0	1		1			KI	152
GA	508		1	0		1			GR	170,0
20	7	0	4	3	7	0	0	7	0	
TA	103		0	1		1			FI	35,0
GC	155		0	1		1			GA	52
GA	245		1	0		1			GE	82
GA	331		1	0		1			DN	111,0
TC	410		1	0		1			LS	137
CA	428		0	1		1			PQ	143

	AG	473		1	0		1		KR	158
21	5		0	5	0	2	2	1	5	0
	GA	265		1	0		1		VI	89,0
	CT	344		1	0		1		PL	115
	GA	396		1	0			1	1 STOP	132
	GA	498		1	0			1	LL	166
	TC	516		1	0			1	AA	172
22	11		0	5	6	10	1	0	11	0
	GT	61		0	1		1		AS	21,0
	CT	120		1	0			1	YY	40
	GC	155		0	1		1		GA	52
	AG	233		1	0		1		DG	78
	AG	284		1	0		1		DG	95
	TA	300		0	1		1		FL	100
	AG	305		0	1		1		EG	102
	CT	377		1	0		1		AV	126
	CG	430		1	0		1		HD	144,0
	AT	466		0	1		1		IF	156,0
	TA	497		0	1		1		LQ	166
23	8		0	6	2	6	2	0	8	0
	TC	84		1	0			1	NN	28
	AG	133		1	0		1		KE	45,0
	CT	146		1	0		1		TI	49
	AG	204		1	0			1	PP	68
	AT	205		0	1		1		TS	69,0
	GT	349		0	1		1		AS	117,0
	AG	460		1	0		1		ND	154,0
	GA	464		1	0		1		GD	155
24	13		0	7	6	8	4	1	13	0
	GC	123		0	1		1		RS	41

AT	191	0	1	1				YF	64
CA	228	0	1	1				FL	76
TC	270	1	0				1	YY	90
TC	300	1	0				1	FF	100
CT	344	1	0			1		PL	115
GA	349	1	0			1		AT	117,0
GA	366	1	0				1	TT	122
CG	377	0	1			1		AG	126
GA	418	1	0			1		DN	140,0
AT	532	0	1					1 STOP	178,0
AG	536	1	0			1		DG	179
AT	540	0	1				1	II	180
25	8	0	5	3	4	4	0	8	0
AT	96	0	1				1	II	32
AG	216	1	0				1	SS	72
CT	219	1	0				1	FF	73
AG	269	1	0			1		YC	90
CT	377	1	0			1		AV	126
GC	444	0	1			1		KN	148
AG	459	1	0				1	TT	153
AT	538	0	1			1		IL	180,0
26	11	0	7	4	5	5	1	11	0
AT	34	0	1					1 STOP	12,0
CT	78	1	0				1	DD	26
TC	114	1	0				1	SS	38
TA	198	0	1			1		FL	66
GA	247	1	0			1		AT	83,0
AG	312	1	0				1	RR	104
TC	323	1	0			1		VA	108
GT	331	0	1			1		DY	111,0

	GA	411		1	0			1		LL	137
	GA	517		1	0		1			VM	173,0
	AT	540		0	1			1		II	180
27	5		2	2	3	3	0	0		5	0
	INSERTION	103		1	0						35,0
	DELETION	225		1	0						75
	GT	349			0		1			AS	117,0
	CT	365			1			1		TM	122
	GA	529			1			1		VM	177,0
28	7		0	2	5	5	2	0		7	0
	GA	60			1				1	RR	20
	GA	65			1					GD	22
	GT	307			0					VL	103,0
	TG	323			0					VG	108
	CG	369			0					SR	123
	AC	429			0				1	PP	143
	GT	500			0					RM	167
29	11		1	2	9	8	2	0		11	0
	TA	48			0				1	AA	16
	GT	57			0					KN	19
	GT	76			0					DY	26,0
	GC	97			0					EQ	33,0
	GC	155			0					GA	52
	TC	179			1					FS	60
	TC	264			1				1	NN	88
	CA	272			0					AD	91
	AT	317			0					KM	106
	DELETION	351			1						117
	TA	539			0					IK	180
30	7		0	4	3	3	3	1		7	0

	CG	62	0	1	1			AG	21	
	TC	84	1	0			1	NN	28	
	CT	240	1	0			1	LL	80	
	TA	266	0	1	1			VD	89	
	AT	341	0	1	1			EV	114	
	CT	369	1	0			1	SS	123	
	GA	396	1	0				1 STOP	132	
31	4		1	1	3	3	0	0	4	0
	DELETION	141	1	0	1					47
	GA	161	1	0	1			GD	54	
	CG	272	0	1	1			AG	91	
	GC	354	0	1	1			LF	118	
33	6		0	2	4	5	1	0	6	0
	AT	125	0	1	1			KM	42	
	CG	149	0	1	1			TR	50	
	TG	190	0	1	1			YD	64,0	
	GA	322	1	0	1			VI	108,0	
	AT	404	0	1	1			KI	135	
	TC	408	1	0			1	AA	136	

TA 13
 AT 33
 CG 8
 GC 17
 TG 3
 GT 12
 GA 37
 AG 29
 CA 7